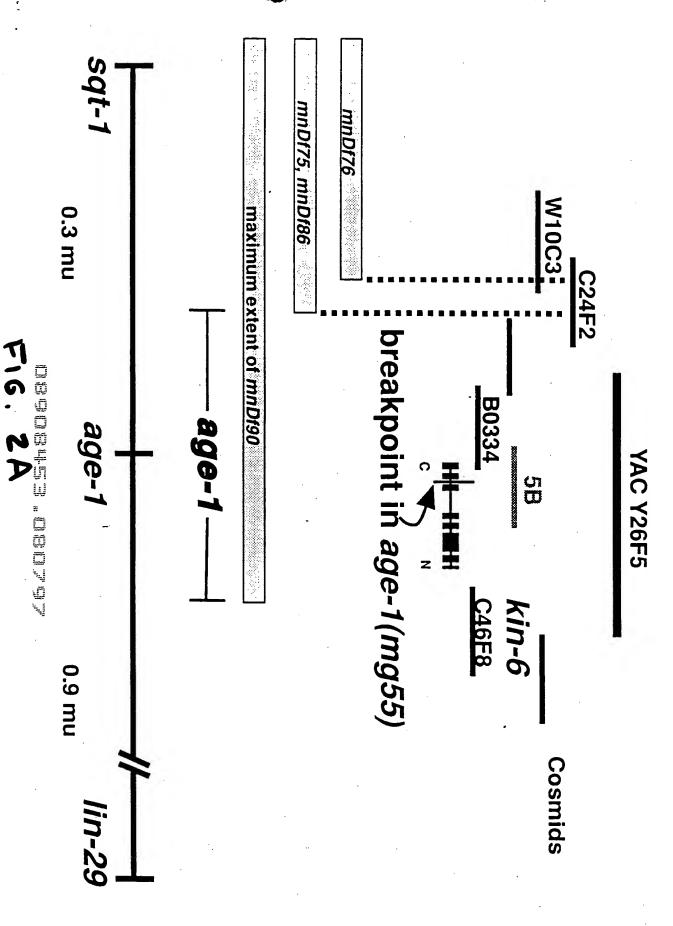


na una 4 **genotype** 

F16. (

# Map of the age-1 Region

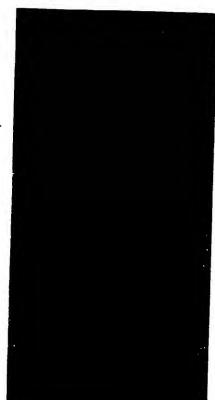


#### Wild-type age-1(mg55)/mnC1 mnDf75/mnC1 mnDf77/mnC1

5.2 kb

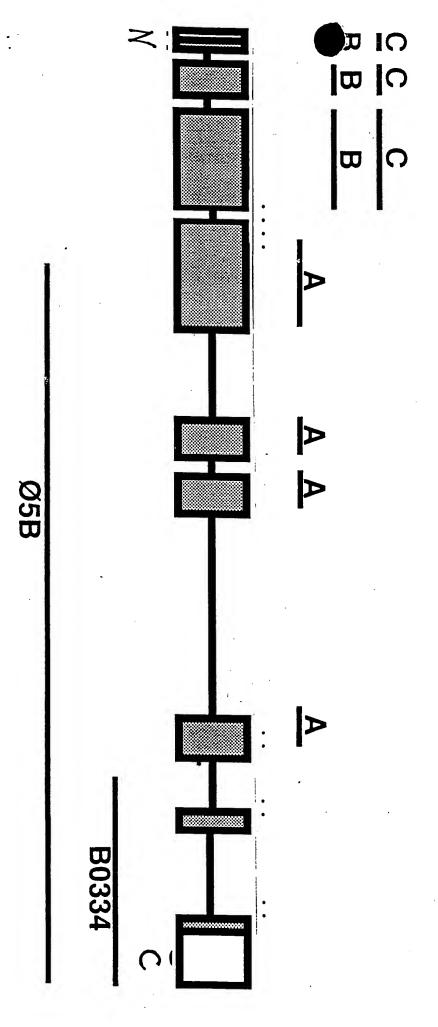
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F16. 2B

## Structure of age-1



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### Fig. 3 (Sheet 2 of 2)

Age-1 Alpha Beta Gamma

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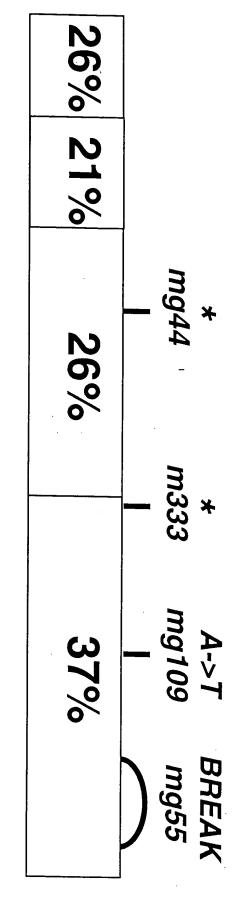
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 121 cgagaacgcc catcgctgga gaccgagaat ggcaaaggat cgctgctcct ggaaaatgaa
 181 qqtqtcqcaq atatcatcac tatgtgtcca ttcggagaag ttattagtgt agtatttccg
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 361 gtgttcagac agttgaataa tttcggcgaa attgaagtta tatttaacga cgatcaaccc
 421 ctqtcqaaat tagagctcca cggcactttc ccaatgcttt ttctctacca acctgatgga
 481 ataaacaggg ataaagaatt aatgagtgat ataagtcatt gtctaggata ctcactggat
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 781 gagaaaatga tgaagattca aattgaattc aatccgaacg aaactccgaa atctctgctt
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2641 cgccaggaca tgcttgttct tcaagttctc gaagttatgg ataacatctg gaaggctgca
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Figure 4 (Sheet 1 of 2)

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Figure 4 (Sheet 1 of 2)

## AND PUTATIVE DOMAINS AGE-1 WITH MUTATIONS



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Unknown

Lipid Kinase

100 a.a.

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F10.5

(SEQ ID NO: 1)

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1 MHVNILHPOL OTMVEQWOMR ERPSLETENG KGSLLLENEG VADIITMCPF
  51 GEVISVVFPW FLANVRTSLE IKLSDFKHQL FELIAPMKWG TYSVKPQDYV
 101 FROLNNFGEI EVIFNDDOPL SKLELHGTFP MLFLYOPDGI NRDKELMSDI
 151 SHCLGYSLDK LEESLDEELR QFRASLWART KKTCLTRGLE GTSHYAFPEE
 201 QYLCVGESCP KDLESKVKAA KLSYQMFWRK RKAEINGVCE KMMKIQIEFN
 251 PNETPKSLLH TFLYEMRKLD VYDTDDPADE GWFLQLAGRT TFVTNPDVKL
 301 TSYDGVRSEL ESYRCPGFVV RRQSLVLKDY CRPKPLYEPH YVRAHERKLA
 351 LDVLSVSIDS TPKQSKNSDM VMTDFRPTAS LKQVSLMDLD ANLMIRPVNI
 401 SGFDFPADVD MYVRIEFSVY VGTLTLASKS TTKVNAQFAK WNKEMYTFDL
 451 YMKDMPPSAV LSIRVLYGKV KLKSEEFEVG WVNMSLTDWR DELROGOFLF
 501 HLWAPEPTAN RSRIGENGAR IGTNAAVTIE ISSYGGRVRM PSQGQYTYLV
 551 KHRSTWTETL NIMGDDYESC IRDPGYKKLO MLVKKHESGI VLEEDEQRHV
 601 WMWRRYIOKO EPDLLIVLSE LAFVWTDREN FSELYVMLEK WKPPSVAAAL
 651 TLLGKRCTDR VIRKFAVEKL NEOLSPVTFH LFILPLIQAL KYEPRAQSEV
 701 GMMLLTRALC DYRIGHRLFW LLRAEIARLR DCDLKSEEYR RISLLMEAYL
 751 RGNEEHIKII TRQVDMVDEL TRISTLVKGM PKDVATMKLR DELRSISHKM
 801 ENMDSPLDPV YKLGEMIIDK AIVLGSAKRP LMLHWKNKNP KSDLHLPFCA
 851 MIFKNGDDLR ODMLVLOVLE VMDNIWKAAN IDCCLNPYAV LPMGEMIGII
 901 EVVPNCKTIF EIQVGTGFMN TAVRSIDPSF MNKWIRKQCG IEDEKKKSKK
 951 DSTKNPIEKK IDNTOAMKKY FESVDRFLYS CVGYSVATYI MGIKDRHSDN
1001 LMLTEDGKYV HIDFGHILGH GKTKLGIORD ROPFILTEHF MTVIRSGKSV
1051 DGNSHELQKF KTLCVEAYEV MWNNRDLFVS LFTLMLGMEL PELSTKADLD
1101 HLKKTLFCNG ESKEEARKFF AGIYEEAFNG SWSTKTNWLF HAVKHY
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Figure 6